



12th European Conference on Fungal Genetics

A nighttime photograph of Seville, Spain. In the foreground, a modern, illuminated architectural structure with a curved, ribbed design is visible. In the background, the city's skyline is lit up, featuring the prominent Giralda tower and other historic buildings. The sky is a deep orange from the setting or rising sun.

BOOK OF ABSTRACTS

Seville (Spain) March 23-27, 2014

CS2.5

DECIPHERING THE ROLE OF THE FLB-APICAL COMPLEX IN ASEXUAL DEVELOPMENT OF ASPERGILLUS**EDUARDO ANTONIO ESPESO**

CIB/CSIC, SPAIN

An intricate signalling pathway mainly involving transcription factors is behind the regulation of *brlA* expression, the central developmental activator of conidiation. In *Aspergilli*, members of this pathway were identified and called upstream developmental activators, UDAs. Along years, our work has shown that the bZIP transcription factor FlbB is a key element in the UDA pathway and its activity is modulated by a precise cellular location and interaction with other Flb (UDA) partners. UDA is not a linear pathway as initially modelled, in this talk we will learn about the molecular mechanism modelling the apical complex formed by FlbE and FlbB, and its role in cellular distribution and transcriptional activity of FlbB. The regulatory and functional relationship between FlbB and FlbB, a bZIP/cMyb connection, being a common regulatory mechanism of development found from fungi to higher eukaryotes. Finally, RNA sequencing has revealed a number of possible targets for FlbB regulation that extends its role above *brlA* regulation.

CS2.6

REGULATION OF MORPHOGENESIS DURING DEVELOPMENT IN THE FILAMENTOUS FUNGUS ASPERGILLUS NIDULANS**STEVEN HARRIS⁽¹⁾, XIANYUN SUN⁽²⁾, SHAOJIE LI⁽²⁾**⁽¹⁾ UNIVERSITY OF NEBRASKA, UNITED STATES, ⁽²⁾ CHINESE ACADEMY OF SCIENCES, CHINA

In the filamentous fungus *Aspergillus nidulans*, the transition from hyphal growth to asexual development is associated with dramatic changes in patterns of cellular morphogenesis and division. These changes enable the formation of airborne conidiophores that culminate in chains of uninucleate spores generated by repeated budding of phialides. Our objective is to characterize the regulatory modules that mediate these morphological changes and to determine how their evolution could account for the differences in conidiophore morphology observed within the Trichocomaceae. In yeast, the transcription factor Ace2 regulates the expression of functions required for cytokinesis and entry into the next cell cycle. Previous studies also report that Ace2 is required for the formation of phialides in *A. fumigatus*. Here, we characterize the *A. nidulans* Ace2 homologue AN4873. We show that it is required for the transition from hyphal to budding growth during conidiophore development. In particular, the absence of AN4873 results in disordered cell cycle progression within phialides and the production of multinucleate cells. We also describe strong genetic interactions that implicate AN4873 and the Cdc42/RacA GTPases as parallel regulators of conidiophore morphology. Lastly, we present preliminary results from RNA-Seq experiments designed to identify potential targets of Ace2. Collectively, our results provide new insight into the regulatory mechanisms that differentially regulate cellular morphogenesis during growth and development in *A. nidulans*.



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